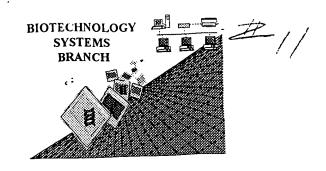
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,465 APR 1 7 2001

Source: 164/ TECH CENTER 1600/2900

Date Processed by STIC: 4/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

| | ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09 | 7554,765 |
|---------------------------------------|--|---|---|-------------------------------------|
| ATTN | : NEW RULES CASES: P | LEASE DISREGARD ENGLISH "ALPHA" | HEADERS, WHICH WERE INSERTED BY F | TO SOFTWARE |
| 1 | : NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. | | | |
| | | This may occur if your file was retrieved in | a word processor after creating it. | Ξ |
| | | Please adjust your right margin to .3, as to | his will prevent "wrapping". | APR CEN |
| 2 | Wrapped Aminos | | each line "wrapped" down to the next line. | 1 7 TER |
| | | This may occur if your file was retrieved in a word processor after creating it. | | |
| | | Please adjust your right margin to .3, as this will prevent "wrapping". | | |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 | characters in length. This includes spaces. | APR 1 7 2001 CH CENTER 1600/2900 |
| 4 | Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs | | | e of tabs |
| | Numbering | between the numbering. It is recommende | ed to delete any tabs and use spacing between | the numbers. |
| 5 | Non-ASCII | This file was not saved in ASCII (DOS) ter | xt, as required by the Sequence Rules. | |
| · · · · · · · · · · · · · · · · · · · | | | on is saved in ASCII text so that it can be proce | essed. |
| 6 | Variable Length | Sequence(s) contain n's or Xaa's wh | ich represented more than one residue | |
| | | As per the rules, each n or Xaa can only re | | |
| | | Please present the maximum number of ea | • | |
| | | indicate in the (ix) feature section that son | ne may be missing. | |
| 7 | Patentin ver. 2.0 "bug" | A "bug" in Patentin version 2.0 has caused | d the <220>-<223> section to be missing from | amino acid |
| | v | sequence(s) Normally, PatentIn would automatically generate this section from the | | |
| | | | Please manually copy the relevant <220>-<223 | |
| | | to the subsequent amino acid sequence. | This applies primarily to the mandatory <2 | 20>-<223> |
| | | sections for Artificial or Unknown sequ | iences. | |
| 8 | Skipped Sequences Sequence(s) missing. If intentional, please use the following form | | please use the following format for each skippe | ed sequence: |
| | (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: | | | |
| | | (i) SEQUENCE CHARACTERISTICS:(Do | o not insert any headings under "SEQUENCE | CHARACTERISTICS") |
| | | (xi) SEQUENCE DESCRIPTION:SEQ ID | | |
| | | This sequence is intentionally skipped | | |
| | | Please also adjust the "(iii) NUMBER OF S | SEQUENCES:" response to include the skippe | ed sequence(s). |
| 9 | Skipped Sequences | | olease use the following format for each skippe | d sequence. |
| | (NEW RULES) | <210> sequence id number | | |
| | | <400> sequence id number | | |
| | | 000 | | |
| 0 | Use of n's or Xaa's | Use of n's and/or Xaa's have been detected | d in the Sequence Listing. | |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY i | f n's or Xaa's are present. | |
| | | In <220> to <223> section, please explain | location of n or Xaa, and which residue n or X | (aa represents. |
| 1 J | Use of "Artificial" | Lise of "Artificial" only as "<213> Organism | n" response is incomplete, per 1,823/h) of Nov | v Saguence Bules |
| ' | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. (NEW RULES) Valid response is Artificial Sequence. | | | 7 Sequence Nules. |
| 2 | Use of <220>Feature | Sequence(s) are missing the <220>F | Feature and associated headings | |
| | (NEW RULES) | _ | f <213>ORGANISM is "Artificial Sequence" or | "Unknown" |
| | • | Please explain source of genetic mater | • | |
| | | | | (Sec. 1.823 of new Rules |
| 3 | Patentin ver. 2.0 "bug" | Please do not use "Conv to Dick" funct | tion of PatentIn version 2.0. This causes a c | comunited |
| | - a.c.mii ver. 2.0 bug | | c identifiers and responses (as indicated on ra | |

AMC - Biotechnology Systems Branch - 4/06/2001

Instead, please use "File Manager" or any other means to copy file to floppy disk.

TIME: 10:40:04

1641

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                                                                      Corrected Diskette Needed
      3 <110> APPLICANT: Kufer, Peter
              Raum, Tobias
                                                                      pp 1-7
              Borschert, Katrin
              Zettl, Florian
              Lutterbuse, Ralf
      9 <120> TITLE OF INVENTION: A novel method of identifying binding site domains that
retain the
     10
              capacity of binding to an epitope
     12 <130> FILE REFERENCE: 147-199P
     14 <140> CURRENT APPLICATION NUMBER: US 09/554,465
     15 <141> CURRENT FILING DATE: 2000-10-19
     17 <150> PRIOR APPLICATION NUMBER: PCT/EP98/07313
     18 <151> PRIOR FILING DATE: 1998-11-16
     20 <160> NUMBER OF SEQ ID NOS: 71
                                    (globalerna)
) see item // on Eva Summary Sheet
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     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 33
     26 <212> TYPE: DNA
     27 <213> ORGANISM: artificial
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     51 <213> ORGANISM: ártificial
     53 <220> FEATURE:
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     56 <400> SEQUENCE: 3
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     63 <213> ORGANISM: artificial
     65 <220> FEATURE:
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17-
     67
              1A antibody M74 V(L
     69 <400> SEQUENCE: 4
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US/09/554,465

RAW SEQUENCE LISTING PATENT APPLICATION:

70 aggtgtacac tccgatatcc agctgaccca gtctcca

37

TIME: 10:40:04

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     83 ggagcegeeg eegeeagaae caccaccace tttgateteg agettggtee e
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     89 <213> ORGANISM:\artificial
     91 <220> FEATURE:
     92 <223> OTHER INFORMATION: primer to single-chain Fv fragment (scFv) of the murine anti
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     93
              A antibody M74 V(H
     95 <400> SEQUENCE: 6
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     98 ctggtgaagc ctggggcttc agtgaagatt tcctgc
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     126 atttcctgc
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     132 <213> ORGANIÉM: artificial
     134 <220> FEATURE:
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     136
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/554,465

144 <210> SEQ ID NO: 10

TIME: 10:40:04

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212 <223> OTHER INFORMATION: primer for V(L) chain of human anti-17-1A antibody

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RAW SEQUENCE LISTING

PATENT APPLICATION:

33

211 <220> FEATURE:

214 <400> SEQUENCE: 15

215 gaagacacta gttgcagcca ccgtacgttt rat

TIME: 10:40:04

Input Set : A:\PTO.txt Output Set: N:\CRF3\04062001\I554465.raw 218 <210> SEQ ID NO: 16 219 <211> LENGTH: 24 220 <212> TYPE: DNA 221 <213> ORGANISM artificial 223 <220> FEATURE: 224 <223> OTHER INFORMATION: oligomer encoding six HIS residues 226 <400> SEQUENCE: 16 24 227 ctagccatca ccatcaccat caca 230 <210> SEQ ID NO: 17 231 <211> LENGTH: 24 232 <212> TYPE: DNA 233 <213> ORGANISM: artificial 235 <220> FEATURE: 236 <223> OTHER INFORMATION: oligomer containing six HIS residues 238 <400> SEQUENCE: 17 24 239 ctagtgtgat ggtgatggtg atgg 242 <210> SEQ ID NO: 18 243 <211> LENGTH: 47 244 <212> TYPE: DNA 245 <213> ORGANISM: (artificial 247 <220> FEATURE: 248 <223> OTHER INFORMATION: oligonucleotide for multiple cloning site containing SacI and Xho 249 I overhang 251 <400> SEQUENCE: 18 252 gcagctggtc gacaaatccg gaggtggtgg atccgaggtg cagctgc 47 255 <210> SEQ ID NO: 19 256 <211> LENGTH: 55 257 <212> TYPE: DNA multiple 258 <213> ORGANISM artificial 260 <220> FEATURE: 261 <223> OTHER INFORMATION: oligonucleotide containing (multple) cloning site with SacI and Xho 262 I overhang 264 <400> SEQUENCE: 19 265 tegageaget geacetegga tecaceacet ceggatttgt egaceagetg eaget 55 268 <210> SEQ ID NO: 20 269 <211> LENGTH: 79 270 <212> TYPE: DNA 271 <213> ORGANISM: artificial 273 <220> FEATURE: 274 <223> OTHER INFORMATION: oligonucleotide containing multiple cloning sites 276 <400> SEQUENCE: 20 277 tegageeegg teacegtete eteaggtggt ggtggttetg geggeggegg eteeggtggt 60 279 ggtggttctg agctcggga 79 282 <210> SEQ ID NO: 21 283 <211> LENGTH: 79

288 <223> OTHER INFORMATION: oligonucleotide containing multiple cloning site

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/554,465

284 <212> TYPE: DNA

287 <220> FEATURE:

285 <213> ORGANISM: artificial

RAW SEQUENCE LISTING

DATE: 04/06/2001 TIME: 10:40:04

PATENT APPLICATION: US/09/554,465

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04062001\I554465.raw

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301 <220> FEATURE:
302 <223> OTHER INFORMATION: primer for M13 gene III domain N2
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308 <210> SEQ TD NO: 23
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325 <220> FEATURE:
326 <223> OTHER INFORMATION: primer for detection of positive clones
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337 <220> FEATURE:
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345 <211> LENGTH: 32
346 <212> TYPE: DNA-
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347 <213> ORGANISM: artificial
349 <220> FEATURE.
350 <223> OTHER INFORMATION: primer for the extracellular region ofthe human CD54 antigen
351
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353 <400> SEQUENCE: 26
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359 <212> TYPE: DNA
360 <213> ORGANISM: artificial
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Subsequent sequences
362 <220> FEATURE
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know

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/554,465

DATE: 04/06/2001 TIME: 10:40:05

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04062001\I554465.raw